AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph at 55:19 - 56:6 with the following amended paragraph:

By using this computational protocol, genome sequence data bases such as maintained by various organizations including: www.tigr.org/tdb; www.genetics.wisc.edu; www.stanford.edu/~ball; hiv-web.lanl.gov; www.ncbi.nlm.nih.gov; www.ebi.ac.uk; pasteur.fr/other/biology; and www.genome.wi.mit.edu, ~~http://www.tigr.org/tdb; http://www.genetics.wisc.edu; http://genome-www.stanford.edu/~ball; http://hiv-web.lanl.gov; http://wwwncbi.nlm.nih.gov; http://www.ebi.ac.uk; http://pasteur.fr/other/biology; and http://www-genome.wi.mit.edu~~, can be rapidly screened for specific protein active sites and for identification of the residues at those active sites which resemble a desired molecule. Several other groups have developed databases of short sequence patterns or motifs designed to identify a given function or activity of a protein. These databases, notably Prosite (expasy.hcuge.ch/sprot/prosite.html; Blocks (www.blocks.fhcrc.org); and Prints (www.biochem.ucl.ac.uk/bsm/dbbrowser/PRINTS/PRINTS.html), ~~(http://expasy.hcuge.ch/sprot/prosite.html); Blocks (http://www.blocks.fhcrc.org); and Prints (http://www.biochem.ucl.ac.uk/bsm/dbbrowser/PRINTS/PRINTS.html)~~, use short stretches of sequence information to identify sequence patterns that are specific for a given function; thus they avoid the problems arising from the necessity of matching entire sequences. In this manner, new FCR3.varCSA modulating agents are rationally selected for further identification by FCR3.varCSA characterization assays, as described above. Rounds or cycles of functional assays on the molecules and derivatives thereof and further FFF refinement and database searching allows an investigator to more narrowly define classes of FCR3.varCSA modulating agents that produce a desired modulation of the formation of a FCR3.varCSA-CSA complex.